

## ABSTRACT

A method of identifying a compound capable of correcting an impaired enzymatic activity of a mutant glucocerebrosidase molecule, the method comprising: (a) obtaining a first set of structure coordinates, the first set of structure coordinates defining a 3D structure of a glucocerebrosidase molecule capable of displaying normal enzymatic activity or a portion thereof; (b) computationally generating using the first set of structure coordinates a second set of structure coordinates, the second set of structure coordinates defining a predicted 3D structure of the mutant glucocerebrosidase molecule or a portion thereof; and (c) computationally identifying, using the second set of structure coordinates, a compound capable of interacting with the mutant glucocerebrosidase molecule in such a way as to correct the impaired enzymatic activity thereof, thereby identifying the compound capable of correcting the impaired enzymatic activity of the mutant glucocerebrosidase molecule. A glucocerebrosidase preparation comprising a population of glucocerebrosidase molecules, wherein substantially each of said glucocerebrosidase molecules: (i) has an amino acid sequence at least 95 percent homologous to an amino acid sequence set forth by SEQ ID NO: 1 or 8; (ii) is glycosylated at, or has an aspartatic acid residue at, glycosylation residue 1 of said amino acid sequence; and (iii) is independently unglycosylated at one or more glycosylation residues selected from the group consisting of glycosylation residues 2, 3 and 4 of said amino acid sequence.